

- 75 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
(B) STREET: OFFICE OF TECHNOLOGY TRANSFER, SUITE 325
6011 EXECUTIVE BOULEVARD
(C) CITY: ROCKVILLE
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 20852

(i) APPLICANT:

(A) NAME: NELSON, EDWARD L.
(B) STREET: 660 BUCKHORN ROAD
(C) CITY: ELDERSBURG
(D) STATE OR PROVINCE: MARYLAND
(E) COUNTRY: UNITED STATES OF AMERICA
(F) POSTAL CODE: 21784

(i) APPLICANT:

(A) NAME: NELSON, PETER J.
(B) STREET: REUTTERSTRASSE 70
(C) CITY: MUNICH
(E) COUNTRY: GERMANY
(F) POSTAL CODE: 80689

(ii) TITLE OF INVENTION: NOVEL VECTOR FOR POLYNUCLEOTIDE VACCINES

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1

092202-109

- 76 -

- (vi) CURRENT APPLICATION DATA:
(A) FILING DATE: 14-AUG-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US60/023931
(B) FILING DATE: 14-AUG-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: KATHRYN M. BROWN
(B) REGISTRATION NUMBER: 34556
(C) REFERENCE/DOCKET NUMBER: 2026-4236PC
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 758-4800
(B) TELEFAX: (212) 751-6849
(C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:1:

GGCCGCGTTG	CTGGCGTTTT	TCCATAGGCT	CCGCCCCCCT	40
GACGAGCATC	ACAAAAATCG	ACGCTCAAGT	CAGAGGTGGC	80
GAAACCCGAC	AGGACTATAA	AGATACCAGG	CGTTTCCCCC	120
TGGAAGCTCC	CTCGTGCGCT	CTCCTGTTCC	GACCCTGCCG	160
CTTACCGGAT	ACCTCTCCGC	CTTTCTCCCT	TCGGGAAGCG	200
TGGCGCTTTC	TCAATGCTCA	CGCIGTAGGT	ATCTCAGTTC	240
GGTGTAGGTC	GTTCGCTCCA	AGCTGGGCTG	TGTGCACGAA	280
CCCCCGCTIC	AGCCCGACCG	CTGCGCCTTA	TCCGGTAACT	320
ATCGTCTTGA	GTCCAACCCG	GTAAGACACG	ACTTATCGCC	360
ACTGGCAGCA	GCCACTGGTA	ACAGGATTAG	CAGAGCGAGG	400
TATGTAGGCG	GTGCTACAGA	GTTCTTGAAG	TGGTGGCCTA	440
ACTACGGCTA	CAC			453

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 453 base pairs
(B) TYPE: nucleic acid

- 77 -

(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:2:

GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	AACTCTGTAG	40
CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	TGTTACCAGT	80
GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	TACCGGGTTG	120
GACTCAAGAC	GATAGTTACC	GGATAAGCG	CAGCGGTCGG	160
GCTGAACGGG	GGGTTCTGTC	ACACAGCCCA	GCTTGGAGCG	200
AACGACCTAC	ACCGAACTGA	GATACCTACA	CCGTGAGCAT	240
TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	AAGGCGGACA	280
GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	GAGAGCGCAC	320
GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	TCTTTATAGT	360
CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	CGTCGATTTT	400
TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	GGAAAAACGC	440
CAGCAACGCG	GCC			453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

GAATTCTTTC	GGACTTTTGA	AAGTGATGGT	GGTGGCCGAA	40
GGATTCGAAC	CTTCGAAGTC	GATGACGGCA	GATTTAGAGT	80
CTGCTCCCTT	TGGCCGCTCG	GGAACCCAC	CACGGGTAAT	120
GCTTTTACTG	GCCTGCTCCC	TTATCGGGAA	GCGGGGCGCA	160
TCATATCAAA	TGACGCGCCG	CTGTAAAGTG	TTACGTTGAG	200
AAAGAATTC				210

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 base pairs

09242202-110199

- 78 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

GAATTCTTTC	TCAACGTAAC	ACTTTACAGC	GGCGCGTCAT	40
TTGATATGAT	GCGCCCCGCT	TCCCGATAAG	GGAGCAGGCC	80
AGTAAAAGCA	TTACCCGTGG	TGGGGTTCCG	GAGCGGCCAA	120
AGGGAGCAGA	CTCTAAATCT	GCCGTCATCG	ACTTCGAAGG	160
TTCGAATCCT	TCCCCACCA	CCATCACTTT	CAAAAGTCCG	200
AAAGAATTC				209

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:5:

AATAAA

6

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:6:

- 79 -

ATTAAA

6

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:7:

AGTAAA

6

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:8:

AAGAAC

6

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No

551011 20224250

- 80 -

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:9:

AATACA

6

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:10:

GCCTTAAGGG	CCATATGGTG	AGTGGATCCC	TTGACCCAG	40
GCGGGGATGG	GGAGACCTG	TAGTCAGAGC	CCCCGGGCAG	80
CACAGGCCAA	TGCCCCGTCCT	TCCCCTGCAG	GATGAGTAGT	120
GAGTGCCTCT	CCTGGCCCTG	GAAGTTGCCA	CTCCAGTGCC	160
CACCAGCCTT	GTCCTAATAA	AATTAAGTTG	CATCATTTTG	200
TCTGACTAGG	TGTCCTCTAT	AATATTAT		228

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:11:

ATAATATTAT	AGAGGACACC	TAGTCAGAAC	AAATGATGCA	40
ACTTAATTTT	ATTAGGACAA	GGCTGGTGGG	CACTGGAGTG	80
GCAACTTCCA	GGGCCAGGAG	AGGCACTCAC	TACTCATCCT	120

66707-20224250

- 81 -

GCAGGGGAAG	GACGGGCATT	GGCCTGTGCT	CCCCGGGGGC	160
TCTGACTACA	GGTCTCCCCC	ATCCCCGCCT	GGGGTCAAGG	200
CATCCACTCA	CCATATGGCC	CTTAAGG		228

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:12:

CCTCGGTACC	TGCCATGGCG	CGGATTCTTT	ATCACTGATA	40
AGTTGGTGGA	CATATTATGT	TTATCAGTGA	TAAAGTGTCA	80
AGCATGACAA	AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	120
GCCCTGGACT	GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	160
GACACGCAA	CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	200
GCGCTTTACT	GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	240
GGCCATATGC	CG			252

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

CCTCGGTACC	TGCCACCATG	GCGCGGATTC	TTTAT	35
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(2) INFORMATION FOR SEQ ID NO:14:

094300 10199

- 82 -

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

CGGCATATGG CCTTAAGGCG CCCGCTTGTT CCTGAAGT

38

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:15:

GCCTTAAGGG	CCATATGGTG	AGTGGATGCC	TTGACCCCAG	40
GCGGGGATGG	GGGAGACCTG	TAGTCAGAGC	CCCCGGGCAG	80
CACAGGCCAA	TGCCCCGTCCT	TCCCCTGCAG	GATGAGTAGT	120
GAGTGCCTCT	CCTGGCCCTG	GAAGTTGCCA	CTCCAGTGCC	160
CACCAGCCTT	GTCCTAATAA	AATTAAGTTG	CATCATTTTG	200
TCTGACTAGG	TGTCCTCTAT	AATATTAT		228

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA

- 83 -

- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:16:

TGCCATGGCG	CGGATTCTTT	ATCACTGATA	AGTTGGTGGA	40
CATATTATGT	TTATCAGTGA	TAAAGTGTC	AGCATGACAA	80
AGTTGCAGCC	GAATACAGTG	ATCCGTGCCG	GCCCTGGACT	120
GTTGAACGAG	GTCGGCGTAG	ACGGTCTGAC	GACACGCAAA	160
CTGGCGGAAC	GGTTGGGGGT	GCAGCAGCCG	GCGCTTTACT	200
GGCACTTCAG	GAACAAGCGG	GCGCCTTAAG	GGCCATATGG	240
TGAGTGGAATG	CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	280
TGTAGTCAGA	GCCCCCGGGC	AGCACAGGCC	AATGCCCCGTC	320
CTTCCCCTGC	AGTGAGTAGT	GACTGCCCGG	GTGGGATCCC	360
TGTGACCCCT	CCCCAGTGCC	TCTCCTGGCC	CTGGAAGTTG	400
CCACTCCAGT	GCCCACCAGC	CTTGTCTTAA	TAAAATTAAG	440
TTGCATCATT	TTGTCTGACT	AGGTGTCCTC	TATAATATTA	480
TAAGCTTGAT	ATCGAATTCT	TTCTCAACGT	AACACTTTAC	520
AGCGGCGCGT	CATTTGATAT	GATGCGCCCC	GCTTCCCGAT	560
AAGGGAGCAG	GCCAGTAAAA	GCATTACCCG	TGGTGGGGTT	600
CCCGAGCGGC	CAAAGGGAGC	AGACTCTAAA	TCTGCCGTCA	640
TCGACTTCGA	AGGTTCTGAAT	CCTTCCCCCA	CCACCATCAC	680
TTTCAAAAGT	CCGAAAGAAT	TCCTGCAGCC	CGTGTAGCCG	720
TAGTTAGGCC	ACCACTTCAA	GAACCTGTGA	GCACCGCCTA	760
CATACCTCGC	TCTGCTAATC	CTGTTACCAG	TGGCTGCTGC	800
CAGTGGCGAT	AAGTCGTGTC	TTACCGGGTT	GGACTCAAGA	840
CGATAGTTAC	CGGATAAGGC	GCAGCGGTCG	GGCTGAACGG	880
GGGGTTCTGT	CACACAGCCC	AGCTTGGAGC	GAACGACCTA	920
CACCGAACTG	AGATACCTAC	AGCGTGAGCA	TTGAGAAAGC	960
GCCACGCTTC	CCGAAGGGAG	AAAGGCGGAC	AGGTATCCGG	1000
TAAGCGGCAG	GGTCGGAACA	GGAGAGCGCA	CGAGGGAGCT	1040
TCCAGGGGGA	AACGCCTGGT	ATCTTTATAG	TCCTGTCGGG	1080
TTTCGCCACC	TCTGACTTGA	GCGTCGATTT	TTGTGATGCT	1120
CGTCAGGGGG	GCGGAGCCTA	TGGAAAAACG	CCAGCAACGC	1160
GGCCGGGGGA	TCCGGAGAGC	TCACTCTAGA	TGAGAGAGCA	1200
GTGAGGGAGA	GACAGAGACT	CGAATTTCCG	GAGCTATTTT	1240
AGTTTTCTTT	TCCGTTTTGT	GCAATTTTAC	TTATGATACC	1280
GGCCAATGCT	TGGTTGCTAT	TTTGGAAACT	CCCCTTAGGG	1320
GATGCCCCCT	AACTGGCCCT	ATAAAGGGCC	AGCCTGAGCT	1360
GCAGAGGATT	CCTGCAGAGG	ATCAAGACAG	CACGTGGACC	1400
TCGCACAGCC	TCTCCACAG	GTACC		1425

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 720 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- 84 -

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:17:

ATGAGCAAG GGCGAGGAAC TGTTCACTGG CGTGGTCCCA 40
ATTCTCGTGG AACTGGATGG CGATGTGAAT GGGCACAAAT 80
TTTCTGTCAG CGGAGAGGGT GAAGGTGATG CCACATACGG 120
AAAGCTCACC CTGAAATTCA TCTGCACCAC TGGAAAGCTC 160
CCTGTGCCAT GGCCAACACT GGTCACCTACC TTCACCTATG 200
GCGTGCAGTG CTTTTCCAGA TACCCAGACC ATATGAACGA 240
GCATGACTTT TTCAAGAGCG CCATGCCCCG GGGCTATGTG 280
CAGGAGAGAA CCATCTTTTT CAAAGATGAC GGGAACTACA 320
AGACCCGCGC TGAAGTCAAG TTCGAAGGTG ACACCCTGGT 360
GAATAGAATC GAGTTGAAGG GCATTGACTT TAAGGAAGAT 400
GGAAACATTC TCGGCCACAA GCTGGAATAC AACTATAACT 440
CCCACAATGT GTACATCATG GCCGACAAGC AAAAGAATGG 480
CATCAAGGTC AACTTCAAGA TCAGACACAA CATTGAGGAT 520
GGATCCGTGC AGCTGGCCGA CCATTATCAA CAGAACACTC 560
CAATCGGCGA CCGCCCTGTG CTCCTCCCAG ACAACAATTA 600
CCTGTCCACC CAGTCTGCCC TGTCTAAAGA TCCCAACGAA 640
AAGAGAGACC ACATGGTCCT GCTGGAGTTT GTGACCGCTG 680
CTGGGATCAC ACATGGCATG GACGAGCTGT ACAAGTGAGC 720

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1911 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:18:

TATGAGCAAG GGCGAGGAAC TGTTCACTGG CGTGGTCCCA 40
ATTCTCGTGG AACTGGATGG CGATGTGAAT GGGCACAAAT 80
TTTCTGTCAG CGGAGAGGGT GAAGGTGATG CCACATACGG 120
AAAGCTCACC CTGAAATTCA TCTGCACCAC TGGAAAGCTC 160
CCTGTGCCAT GGCCAACACT GGTCACCTACC TTCACCTATG 200
GCGTGCAGTG CTTTTCCAGA TACCCAGACC ATATGAAGCA 240
GCATGACTTT TTCAAGAGCG CCATGCCCCG GGGCTATGTG 280

- 85 -

CAGGAGAGAA CCATCTTTTT CAAAGATGAC GGGA ACTACA 320
 AGACCCGCGC TGAAGTCAAG TTCGAAGGTG ACACCCTGGT 360
 GAATAGAATC GAGTTGAAGG GCATTGACTT TAAGGAAGAT 400
 GGAAACATTC TCGGCCACAA GCTGGAATAC AACTATAACT 440
 CCCACAATGT GTACATCATG GCCGACAAGC AAAAGAATGG 480
 CATCAAGGTC AACTTCAAGA TCAGACACAA CATTGAGGAT 520
 GGATCCGTGC AGCTGGCCGA CCATTATCAA CAGAACACTC 560
 CAATCGGCCA CGGCCCTGTG CTCCTCCAG ACAACCATTA 600
 CCTGTCCACC CAGTCTGCCC GTCTAAAGAT CCCAACGAAA 640
 AGAGAGACCA CATGGTCCTG CTGGAGTTTG TGACCGCTGC 680
 TGGGATCACA CATGGCATGG ACGAGCTGTA CAAGTGAGCC 720
 ATATGGTGAG TGGATGCCTT GACCCAGGC GGGGATGGGG 760
 GAGACCTGTA GTCAGAGCCC CCGGGCAGCA CAGGCCAATG 800
 CCCGTCCTTC CCCTGCAGTG AGTAGTGACT GCCCGGGTGG 840
 GATCCCTGTG ACCCCTCCCC AGTGCCTCTC CTGGCCCTGG 880
 AAGTTGCCAC TCCAGTGCCC ACCAGCCTTG TCCTAATAAA 920
 ATTAAGTTGC ATCATTTTGT CTGACTAGGT GTCCTCTATA 960
 ATATTATAAG CTTGATATCG AATTCTTTCT CAACGTAACA 1000
 CTTTACAGCG GCGCGTCATT TGATATGATG CGCCCCGCTT 1040
 CCCGATAAGG GAGCAGGCCA GTAAAAGCAT TACCCGTGGT 1080
 GGGGTTCCCG AGCGGCCAAA GGGAGCAGAC TCTAAATCTG 1120
 CCGTCATCGA CTTCAAGGT TCGAATCCTT CCCCCACCAC 1160
 CATCACTTTC AAAAGTCCGA AAGAATTCCT GCAGCCCGTG 1200
 TAGCCGTAGT TAGGCCACCA CTTCAAGAAC TCTGTAGCAC 1240
 CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 1280
 TGCTGCCAGT GGCGATAAGT CGTGTCTTAC CGGGTTGGAC 1320
 TCAAGACGAT AGTTACCGGA TAAGGCGCAG CGGTCGGGCT 1360
 GAACGGGGGG TTCGTGCACA CAGCCAGCT TGGAGCGAAC 1400
 GACCTACACC GAACTGAGAT ACCTACAGCG TGAGCATTGA 1440
 GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 1480
 ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG 1520
 GGAGCTTCCA GGGGGAACG CCTGGTATCT TTATAGTCCT 1560
 GTCGGGTTTC GCCACCTCTG ACTTGAGCGT CGATTTTTGT 1600
 GATGCTCGTC AGGGGGGCGG AGCCTATGGA AAAACGCCAG 1640
 CAACGCGGCC GGGGGATCCG GAGAGCTCAC TCTAGATGAG 1680
 AGAGCAGTGA GGGAGAGACA GAGACTCGAA TTTCCGGAGC 1720
 TATTTCAGTT TTCTTTTCCG TTTTGTGCAA TTTCACTTAT 1760
 GATACCGGCC AATGCTTGGT TGCTATTTTG GAAACTCCCC 1800
 TTAGGGGATG CCCCTCAACT GGCCCTATAA AGGGCCAGCC 1840
 TGAGCTGCAG AGGATTCTTG CAGAGGATCA AGACAGCACG 1880
 TGGACCTCGC ACAGCCTCTC CCACAGGTAC C 1911

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

- 86 -

Pro Asp Leu Ser Tyr Met Pro Ile Trp Lys Phe Pro
 1 5 10
 Asp Glu Glu Gly Ala Cys Gln Pro Cys Pro Ile Asn
 15 20
 Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys Gly
 25 30 35
 Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser
 40 45
 Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
 50 55 60
 Val Leu Gly Val Val Phe Gly Ile Leu
 65

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:20:

Pro Ala Pro Gly Ala Gly Gly Met Val His His Arg
 1 5 10
 His Arg Ser Ser Thr Arg Ser Gly Gly Gly Asp
 15 20
 Leu Thr Leu Gly Leu Glu Pro Ser Glu Glu Glu Ala
 25 30 35
 Pro Arg Ser Pro Leu Ala Pro Ser Glu Gly Ala Gly
 40 45
 Ser Asp Val Phe Asp Gly Asp Leu Gly Met Gly Ala
 50 55 60
 Ala Lys Gly Leu Ser Leu Pro Thr His Asp Pro Ser
 65 70
 Pro Leu Gln Arg Tyr Ser Glu Asp Pro Thr Val Pro
 75 80
 Leu Pro Ser Glu Thr Asp Gly Tyr Val Ala Pro Leu
 85 90 95
 Thr Cys Ser Pro Gln Pro Glu Tyr Val Asn Gln Pro
 100 105
 Asp Val Arg Pro Pro Pro Ser Pro Arg Glu Gly Pro
 110 115 120
 Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
 125 130
 Arg Pro Lys Thr Leu Ser Pro Gly Lys Asn Gly Val
 135 140

56707-2024260

- 87 -

Val Lys Asp Val Phe Ala Phe Gly Gly Ala Val Glu
 145 150 155
 Asn Pro Glu Tyr Leu Thr Pro Gln Gly Thr Cys Ser
 160 165
 Pro Gln Pro Glu Tyr Val Asn Gln Pro Asp Val Arg
 170 175 180
 Pro Gln Pro Pro Ser Pro Arg Glu Gly Pro Leu Pro
 185 190
 Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu Arg Pro
 195 200
 Lys Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp
 205 210 215
 Val Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu
 220 225
 Tyr Leu Thr Pro Gln Gly Gly Ala Ala Pro Gln Pro
 230 235 240
 His Pro Pro Pro Ala Phe Ser Pro Ala Phe Asp Asn
 245 250
 Leu Tyr Tyr Trp Asp Asp Pro Pro Glu Arg Gly Ala
 255 260
 Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu
 260 270 275
 Asn Pro Glu Tyr Leu Gly Leu Asp Val Pro Val
 280 285

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:21:

Ile Ile Ser Ala Val Val Gly Ile Leu Leu Val Val
 1 5 10
 Val Leu Gly Val Val Phe Gly Ile Leu Ile
 15 20

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

66T00T" 20224260

- 88 -

- (ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: No
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

66707T 20224260

GCCACCATGG	CCCCTGACCT	CTCCTACATG	CCCATCTGGA	40
AGTTTCCAGA	TGAGGAGGGC	GCATGCCAGC	CTTGCCCCAT	80
CAACTGCACC	CACTCCTGTG	TGGACCTGGA	TGACAAGGGC	120
TGCCCCGCCG	AGCAGAGAGC	CAGCCCTCTG	ACGTCCATCA	160
TCTCTGCGGT	GGTTGGCATT	CTGCTGGTCG	TGGTCTTGGG	200
GGTGGTCTTT	GGGATCCTCA	TCAAGCGACG	GCAGCAGAAG	240
ATCACATGTC	CAGACCCTGC	CCCGGGCGCT	GGGGGCATGG	280
TCCACCACAG	GCACCGCAGC	TCATCTACCA	GGAGTGCGGG	320
TGGGGACCTG	ACACTAGGGC	TGGAGCCCTC	TGAAGAGGAG	360
GCCCCCAGGT	CTCCACTGGC	ACCCTCCGAA	GGGGCTGGCT	400
CCGATGTATT	TGATGGTGAC	CTGGGAATGG	GGGCAGCCAA	440
GGGGCTGCAA	AGCCTCCCCA	CACATGACCC	CAGCCCTCTA	480
CAGCGGTACA	GTGAGGACCC	CACAGTACCC	CTGCCCTCTG	520
AGACTGATGG	CTACGTTGCC	CCCCTGACCT	GCAGCCCCCA	560
GCCTGAATAT	GTGAACCAGC	CAGATGTTCC	GCCCCAGCCC	600
CCTTCGCCCC	GAGAGGGCCC	TCTGCCTGCT	GCCCCGACCTG	640
CTGGTGCCAC	TCTGGAAAGG	CCCAAGACTC	TCTCCCCCAGG	680
GAAGAATGGG	GTCTGCAAAG	ACGTTTTTGC	CTTTGGGGGT	720
GCCGTGGAGA	ACCCCGAGAC	TTGACACCCC	AGGGAGGAGC	760
TGCCCCCTCAG	CCCCACCCTC	CTCCTGCCTT	CAGCCCAGCC	800
TTCGACAACC	TCTATTACTG	GGACCAGGAC	CCACCAGAGC	840
GGGGGGCTCC	ACCCAGCACC	TTCAAAGGGA	CACCTACGGC	880
AGAGAACCCA	GAGTACCTGG	GTCTGGACGT	GCCAGTGTGA	920
AGCCTTAAGG	GCCATATGGT	GAGTGGATGC	CTTGACCCCA	960
GGCGGGGATG	GGGGAGACCT	GTAGTCAGAG	CCCCCGGGCA	1000
GCACAGGCCA	ATGCCCGTCC	TTCCCCTGCA	GTGAGTAGTG	1040
ACTGCCCGGG	TGGGATCCCT	GTGACCCCTC	CCCAGTGCCT	1080
CTCCTGGCCC	TGGAAGTTGC	CACTCCAGTG	CCCACCAGCC	1120
TTGTCCTAAT	AAAATTAAGT	TGCATCATTT	TGTCTGACTA	1160
GGTGTCTCT	ATAATATTAT	AAGCTTGATA	TCGAATTCTT	1200
TCTCAACGTA	ACACTTTACA	GCGGCGCGTC	ATTTGATATG	1240
ATGCGCCCCG	CTTCCCGATA	AGGGAGCAGG	CCAGTAAAAG	1280
CATTACCCGT	GGTGGGGTTC	CCGAGCGGCC	AAAGGGAGCA	1320
GACTCTAAAT	CTGCCGTCAT	CGACTTCGAA	GGTTCGAATC	1360
CTTCCCCCAC	CACCATCACT	TTCAAAAGTC	CGAAAGAATT	1400
CCTGCAGCCC	GTGTAGCCGT	AGTTAGGCCA	CCACTTCAAG	1440
AACTCTGTAG	CACCGCCTAC	ATACCTCGCT	CTGCTAATCC	1480
TGTTACCAGT	GGCTGCTGCC	AGTGGCGATA	AGTCGTGTCT	1520
TACCGGGTTG	GACTIONAGAC	GATAGTTACC	GGATAAGGCG	1560
CAGCGGTCCG	GCTGAACGGG	GGGTTCGTGC	ACACAGCCCA	1600
GCTTGGAGCG	AACGACCTAC	ACCGAACTGA	GATACCTACA	1640
GCGTGAGCAT	TGAGAAAGCG	CCACGCTTCC	CGAAGGGAGA	1680
AAGGCGGACA	GGTATCCGGT	AAGCGGCAGG	GTCGGAACAG	1720
GAGAGCGCAC	GAGGGAGCTT	CCAGGGGGAA	ACGCCTGGTA	1760

- 89 -

TCTTTATAGT	CCTGTCGGGT	TTCGCCACCT	CTGACTTGAG	1820
CGTCGATTTT	TGTGATGCTC	GTCAGGGGGG	CGGAGCCTAT	1860
GGAAAAACGC	CAGCAACGCG	GCCGGGGGAT	CCGGAGAGCT	1900
CACTCTAGAT	GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	1940
GAATTTCCGG	AGCTATTTCA	GTTTTCTTTT	CCGTTTTGTG	1980
CAATTTCACT	TATGATACCG	GCCAATGCTT	GGTTGCTATT	2020
TTGGAAACTC	CCCTTAGGGG	ATGCCCCTCA	ACTGGCCCTA	2060
TAAAGGGCCA	GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	2100
TCAAGACAGC	ACGTGGACCT	CGCACAGCCT	CTCCCACAGG	2140
TACCT				2145

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:23:

GTCTGCCACC ATGGCCTACT CCCCTGC

27

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:24:

TTCTTTGGTG ACCTACCTCT TCGGAATTGC CGAGTC

36

(2) INFORMATION FOR SEQ ID NO:25:

- 90 -

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC 40
 TGAGTCAGGA AACATTTTCA GACCTATGGA AACTACTTCC 80
 TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG 120
 GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT 160
 TCACTGAAGA CCCAGGTCCA GATGAAGCTC CCAGAATGCC 200
 AGAGGCTGCT CCCCGCGTGG CCCCTGCACC AGCAGCTCCT 240
 ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT 280
 CATCTTCTGT CCCTTCCCAG AAAACCTACC AGGGCAGCTA 320
 CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG 360
 TCTGCCACCA TGGCCTACTC CCCTGCGTCT GTGACTTGCA 400
 CGTACTCCCC TGCCCTCAAC AAGATGTTTT GCCAACTGGC 440
 CAAGACCTGC CCTGTGCAGC TGTGGGTTGA TTCCACACCC 480
 CCGCCCGGCA CCCGCGTCCG CGCCATGGCC ATCTACAAGC 520
 AGTCACAGCA CATGACGGAG GTTGTGAGGC GCTGCCCCCA 560
 CCATGAGCGC TGCTCAGATA GCGATGGTCT GGCCCCCTCCT 600
 CAGCGTCTTA TCCGAGTGGA AGGAAATTTG CGTGTGGAGT 640
 ATTTGGATGA CAGAAACACT TTTCGACATA GTGTGGTGGT 680
 GCCCTATGAG CCGCCTGAGG TTGGCTCTGA CTGTACCACC 720
 ATCCACTACA ACTACATGTG TAACAGTTCC TGCATGGGCG 760
 GCATGAACCG GAGGCCCATC CTCACCATCA TCACACTGGA 800
 AGACTCCAGT GGTAAATCTAC TGGGACGGAA CAGCTTTGAG 840
 GTGCGTGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG 880
 AGGAAGAGAA TCTCCGCAAG AAAGGGGAGC CTCACCACGA 920
 GCTGCCCCCA GGGAGCACTA AGCGAGCACT GCCCAACAAC 960
 ACCAGCTCCT CTCCCCAGCC AAAGAAGAAA CCACTGGATG 1000
 GAGAATATTT CACCCTTCAG ATCCGTGGGC GTGAGCGCTT 1040
 CGAGATGTTT TTTGGTGACC TACCTCTTCG GAATTGCCGA 1080
 GTCTTCCGAG AGCTGAATGA GGCCTTGGA CTCAAGGATG 1120
 CCCAGGCTGG GAAGGAGCCA GGGGGGAGCA GGGCTCACTC 1160
 CAGCCACCTG AAGTCCAAAA AGGGTCAGTC TACCTCCCGC 1200
 CATAAAAAAC TCATGTTCAA GACAGAAGGG CCTGACTCAG 1240
 AC 1242

(2) INFORMATION FOR SEQ ID NO:26:

- 91 -

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 608 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:26:

CTCGGGCCGC GTTGCTGGCG TTTTTCATA GGCTCCGCCC 40
CCCTGACGAG CATCACAAA ATCGACGCTC AAGTCAGAGG 80
TGGCGAAACC CGACAGGACT ATAAAGATAC CAGGCGTTTC 120
CCCCTGGAAG CTCCCTCGTG CGCTCTCCTG TTCCGACCCT 160
GCCGCTTACC GGATACCTGT CCGCCTTTCT CCCTTCGGGA 200
AGCGTGGCGC TTTCTCAATG CTCACGCTGT AGGTATCTCA 240
GTTTCGGTGTA GGTCGTTTCG TCCAAGCTGG GCTGTGTGCA 280
CGAACCCCCC GTTCAGCCCG ACCGCTGCGC CTTATCCGGT 320
AACTATCGTC TTGAGTCCAA CCCGGTAAGA CACGACTTAT 360
CGCCACTGGC AGCAGCCACT GGTAACAGGA TTAGCAGAGC 400
GAGGTATGTA GCGGGTGCTA CAGAGTTCTT GAAGTGGTGG 440
CCTAACTACG GCTACACTAG AAGGACAGTA TTTGGTATCT 480
GCGCTCTGCT GAAGCCAGTT ACCTTCGGAA AAAGAGTTGG 520
TAGCTCTTGA TCCGGCAAAC AAACCACCGC TGGTAGCGGT 560
GGTTTTTTTG TTTGCAAGCA GCAGATTACG CGCAGAAAAA 600
AAGGATCT 608

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1547 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION:SEQ ID NO:27:

GGTACCTGCC ACCATGGCGC GGATTCTTTA TCACTGATAA 40
GTTGGTGAC ATATTATGTT TATCAGTGAT AAAGTGTCAA 80
GCATGACAAA GTTGCAGCCG AATACAGTGA TCCGTGCCGG 120

- 92 -

CCCTGGACTG TTGAACGAGG TCGGCGTAGA CGGTCTGACG 160
 ACACGCAAAC TGGCGGAACG GTTGGGGGTG CAGCAGCCGG 200
 CGCTTTACTG GCACTTCAGG AACAAAGCGGG CGCCTTAAGG 240
 GCCATATGGT GAGTGGATGC CTTGACCCCA GGCGGGGATG 280
 GGGGAGACCT GTAGTCAGAG CCCCCGGGCA GCACAGGCCA 320
 ATGCCCCGTC TTCCCCTGCA GGATGAGTAG TGAGTGCCTC 360
 TCCTGGCCCT GGAAGTTGCC ACTCCAGTGC CCACCAGCCT 400
 TGTCTAATA AAATTAAGTT GCATCATTTT GTCTGACTAG 440
 GTGTCCTCTA TAATATTATA AGCTTGATAT CGAATTCTTT 480
 CGGACTTTTG AAAGTGATGG TGGTGGGGGA AGGATTCGAA 520
 CCTTCGAAGT CGATGACGGC AGATTTAGAG TCTGCTCCCT 560
 TTGGCCGCTC GGGAACCCCA CCACGGGTAA TGCTTTTACT 600
 GGCCTGCTCC CTTATCGGGA AGCGGGGCGC ATCATATCAA 640
 ATGACGCGCC GCTGTAAAGT GTTACGTTGA GAAAGAATTC 680
 CTGCAGCCCG CCGCGTTGCT GCGGTTTTTC CATAGGCTCC 720
 GCCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA 760
 GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG 800
 TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA 840
 CCCTGGCCGT TACCGGATAC CTGTCCGCCT TTCTCCCTTC 880
 GGGAAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT 920
 CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG 960
 TGCACGAACC CCCC GTTCAG CCCGACCGCT GCGCCTTATC 1000
 CGGTAACAT CGTCTTGAGT CCAACCCGGT AAGACACGAC 1040
 TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA 1080
 GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG 1120
 GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT 1160
 ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG 1200
 TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG 1240
 CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA 1280
 AAAAAAGGAT CTGGGGGATC CGGAGAGCTC ACTCTAGATG 1320
 AGAGAGCAGT GAGGGAGAGA CAGAGACTCG AATTTCCGGA 1360
 GCTATTTTCA TTTTCTTTTC CGTTTTGTAT AATTTCACTT 1400
 ATGATACCGG CCAATGCTTG GTTGCTATTT TGGAAACTCC 1440
 CCTTAGGGGA TGCCCCTCAA CTGGCCCTAT AAAGGGCCAG 1480
 CCTGAGCTGC AGAGGATTCC TGCAGAGGAT CAAGACAGCA 1520
 CGTGGACCTC GCACAGCCTC TCCCACA 1547

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: No
- (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

- 93 -

GGTACCTGCC ACCATGGCGC GGATTCTTTA TCACTGATAA 40
GTTGGTGGAC ATATTATGTT TATCAGTGAT AAAGTGTCAG 80
GCATGACAAA GTTGCAGCCG AATACAGTGA TCCGTGCCGG 120
CCCTGGACTG TTGAACGAGG TCGGCGTAGA CGGTCTGACG 160
ACACGCAAAC TGGCGGAACG GTTGGGGGTG CAGCAGCCGG 200
CGCTTTACTG GCACTTCAGG AACAAGCGGG CGCCTTAAGG 240
GCCATATGGT GAGTGGATGC CTTGACCCCA GGCGGGGATG 280
GGGGAGACCT GTAGTCAGAG CCCCCGGGCA GCACAGGCCA 320
ATGCCCCGTC TTCCCCTGCA GGATGAGTAG TGAGTGCCTC 360
TCCTGGCCCT GGAAGTTGCC ACTCCAGTGC CCACCAGCCT 400
TGTCCTAATA AAATTAAGTT GCATCATTTT GTCTGACTAG 440
GTGTCCTCTA TAATATTATA AGCTTGATAT CGAATTCTTT 480
CGGACTTTTG AAAGTGATGG TGGTGGGGGA AGGATTCGAA 520
CCTTCGAAGT CGATGACGGC AGATTTAGAG TCTGCTCCCT 560
TTGGCCGCTC GGGAACCCCA CCACGGGTAA TGCTTTTACT 600
GGCCTGCTCC CTTATCGGGA AGCGGGGCGC ATCATATCAA 640
ATGACGCGCC GCTGTAAAGT GTTACGTTGA GAAAGAATTC 680
CTGCAGCCCG CCGCGTTGCT GGCCTTTTTT CATAGGCTCC 720
GCCCCCTGA CGAGCATCAC AAAAATCGAC GCTCAAGTCA 760
GAGGTGGCGA AACCCGACAG GACTATAAAG ATACCAGGCG 800
TTTCCCCCTG GAAGCTCCCT CGTGCGCTCT CCTGTTCCGA 840
CCCTGCCGCT TACCGGATAC CTGTCCGCCT TTCTCCCTTC 880
GGGAAGCGTG GCGCTTTCTC AATGCTCACG CTGTAGGTAT 920
CTCAGTTCGG TGTAGGTCGT TCGCTCCAAG CTGGGCTGTG 960
TGCACGAACC CCCCCTTCAG CCCGACCGCT GCGCCTTATC 1000
CGGTAACAT CGTCTTGAGT CCAACCCGGT AAGACACGAC 1040
TTATCGCCAC TGGCAGCAGC CACTGGTAAC AGGATTAGCA 1080
GAGCGAGGTA TGTAGGCGGT GCTACAGAGT TCTTGAAGTG 1120
GTGGCCTAAC TACGGCTACA CTAGAAGGAC AGTATTTGGT 1160
ATCTGCGCTC TGCTGAAGCC AGTTACCTTC GGAAAAAGAG 1200
TTGGTAGCTC TTGATCCGGC AAACAAACCA CCGCTGGTAG 1240
CGGTGGTTTT TTTGTTTGCA AGCAGCAGAT TACGCGCAGA 1280
AAAAAAGGAT CTGGGGGATC CGGAGAGCTC CCAACGCGTT 1320
GGATGCATGG ATGAGGGAAA GGAGGTAAGA TCTGTAATGA 1400
ATAAGCAGGA ACTTTGAAGA CTCAGTGAAT CAGTGAGTAA 1440
TAAAGACTCA GTGACTTCTG ATCCTGTCCT AACTGCCACT 1480
CCTTGTTGTC CCAAGAAAGC GGCTTCCTGC TCTCTGAGGA 1520
GGACCCCTTC CCTGGAAGGT AAAACTAAGG ATGTCAGCAG 1560
AGAAATTTTT CCACCATTGG TGCTTGGTCA AAGAGGAAAC 1600
TGATGAGCTC ACTCTAGATG AGAGAGCAGT GAGGGAGAGA 1640
CAGAGACTCG AATTTCCGGA GCTATTTTCA TTTTCTTTTC 1680
CGTTTTGTGC AATTTCACTT ATGATACCGG CCAATGCTTG 1720
GTTGCTATTT TGGAAACTCC CCTTAGGGGA TGCCCTCAA 1760
CTGGCCCTAT AAAGGGCCAG CCTGAGCTGC AGAGGATTCC 1800
TGCAGAGGAT CAAGACAGCA CGTGACCTC GCACAGCCTC 1840
TCCCACA 1847

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- 94 -

(A) LENGTH: 2308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGTACCTGCC	ACCATGGCGA	AGGGCGAGGA	ACTGTTCACT	40
GGCGTGGTCC	CAATTCTCGT	GGAAGTGGAT	GGCGATGTGA	80
ATGGGCACAA	ATTTTCTGTC	AGCGGAGAGG	GTGAAGGTGA	120
TGCCACATAC	GGAAAGCTCA	CCCTGAAATT	CATCTGCACC	160
ACTGGAAAGC	TCCCTGTGCC	ATGGCCAACA	CTGGTCACTA	200
CCTTCACCTA	TGGCGTGCAG	TGCTTTTCCA	GATACCCAGA	240
CCATATGAAG	CAGCATGACT	TTTTCAAGAG	CGCCATGCCC	280
GAGGGCTATG	TGCAGGAGAG	AACCATCTTT	TTCAAAGATG	320
ACGGGAACCTA	CAAGACCCGC	GCTGAAGTCA	AGTTCGAAGG	360
TGACACCCTG	GTGAATAGAA	TCGAGTTGAA	GGGCATTGAC	400
TTTAAGGAAG	ATGGAAACAT	TCTCGGCCAC	AAGCTGGAAT	440
ACAACTATAA	CTCCCACAAT	GTGTACATCA	TGGCCGACAA	480
GCAAAAGAAT	GGCATCAAGG	TCAACTTCAA	GATCAGACAC	520
AACATTGAGG	ATGGATCCGT	GCAGCTGGCC	GACCATTATC	560
AACAGAACAC	TCCAATCGGC	GACGGCCCTG	TGCTCCTCCC	600
AGACAACCAT	TACCTGTCCA	CCCAGTCTGC	CCTGTCTAAA	640
GATCCCAACG	AAAAGAGAGA	CCACATGGTC	CTGCTGGAGT	680
TTGTGACCGC	TGCTGGGATC	ACACATGGCA	TGGACGAGCT	720
GTACAAAGTGA	GCGCCTTAAG	GGCCATATGG	TGAGTGGATG	760
CCTTGACCCC	AGGCGGGGAT	GGGGGAGACC	TGTAGTCAGA	800
GCCCCCGGGC	AGCACAGGCC	AATGCCCGTC	CTTCCCCTGC	840
AGGATGAGTA	GTGAGTGCCT	CTCCTGGCCC	TGGAAGTTGC	880
CACTCCAGTG	CCCACCAGCC	TTGTCCTAAT	AAAATTAAGT	920
TGCATCATTT	TGTCTGACTA	GGTGTCTCT	ATAATATTAT	960
AAGCTTGATA	TCGAATTCTT	TCGGACTTTT	GAAAGTGATG	1000
GTGGTGGGGG	AAGGATTCGA	ACCTTCGAAG	TCGATGACGG	1040
CAGATTTAGA	GTCTGCTCCC	TTTGGCCGCT	CGGGAACCCC	1080
ACCACGGGTA	ATGCTTTTAC	TGGCCTGCTC	CCTTATCGGG	1120
AAGCGGGGCG	CATCATATCA	AATGACGCGC	CGCTGTAAAG	1160
TGTTACGTTG	AGAAAGAATT	CCTGCAGCCC	GCCGCGTTGC	1200
TGGCGTTTTT	CCATAGGCTC	CGCCCCCTG	ACGAGCATCA	1240
CAAAAATCGA	CGCTCAAGTC	AGAGGTGGCG	AAACCCGACA	1280
GGACTATAAA	GATACCAGGC	GTTTCCCCCT	GGAAGCTCCC	1320
TCGTGCGCTC	TCCTGTTCCG	ACCCTGCCGC	TTACCGGATA	1360
CCTGTCCGCC	TTTCTCCCTT	CGGGAAGCGT	GGCGCTTTCT	1400
CAATGCTCAC	GCTGTAGGTA	TCTCAGTTCT	GTGTAGGTCT	1440
TTCTGCTCAA	GCTGGGCTGT	GTGCACGAAC	CCCCCGTTCA	1480
GCCCGACCGC	TGCGCCTTAT	CCGGTAACTA	TCGTCTTGAG	1520
TCCAACCCGG	TAAGACACGA	CTTATCGCCA	CTGGCAGCAG	1560

651011 = 202424250

- 95 -

CCACTGGTAA	CAGGATTAGC	AGAGCGAGGT	ATGTAGGCGG	1600
TGCTACAGAG	TTCTTGAAGT	GGTGGCCTAA	CTACGGCTAC	1640
ACTAGAAGGA	CAGTATTTGG	TATCTGCGCT	CTGCTGAAGC	1680
CAGTTACCTT	CGGAAAAAGA	GTTGGTAGCT	CTTGATCCGG	1720
CAAACAAACC	ACCGCTGGTA	GCGGTGGTTT	TTTTGTTTGC	1760
AAGCAGCAGA	TTACGCGCAG	AAAAAAAGGA	TCTGGGGGAT	1800
CCGGAGAGCT	CCCAACGCGT	TGGATGCATG	GATGAGGGAA	1840
AGGAGGTAAG	ATCTGTAATG	AATAAGCAGG	AACTTTGAAG	1880
ACTCAGTGAC	TCAGTGAGTA	ATAAAGACTC	AGTGACTTCT	1920
GATCCTGTCC	TAACTGCCAC	TCCTTGTTGT	CCCAAGAAAG	1960
CGGCTTCCTG	CTCTCTGAGG	AGGACCCCTT	CCCTGGAAGG	2000
TAAAACTAAG	GATGTCAGCA	GAGAAATTTT	TCCACCATTG	2040
GTGCTTGGTC	AAAGAGGAAA	CTGATGAGCT	CACTCTAGAT	2080
GAGAGAGCAG	TGAGGGAGAG	ACAGAGACTC	GAATTTCCGG	2120
AGCTATTTCA	GTTTTCTTTT	CCGTTTTGTG	CAATTTCACT	2160
TATGATACCG	GCCAATGCTT	GGTTGCTATT	TTGGAAACTC	2200
CCCTTAGGGG	ATGCCCCCTCA	ACTGGCCCTA	TAAAGGGCCA	2240
GCCTGAGCTG	CAGAGGATTC	CTGCAGAGGA	TCAAGACAGC	2280
ACGTGGACCT	CGCACAGCCT	CTCCCACA		2308

66T0T 2024260